STIC-Biotech/Ch mLib

61786

Fr m: STIC-ILL
Sent: Wednesday, March 06, 2002 9:19 AM
T : STIC-Biotech/ChemLib
Subject: FW: sequence search request

-----Original Message-----
From: Chernyshev, Olga
Sent: Wednesday, March 06, 2002 9:17 AM
To: STIC-ILL
Subject: sequence search request

US case 09/853,753
Please search SEQ ID NO:1 and 2.
Thank you very much!

Olga N. Chernyshev
AU1646
CM1 8D06
305-1003
mail box 10C01

Edward Hart
Technical Info. Specialist
STIC/Biotech
CMI 6B02 Tel: 305-9203

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: 3/7/02
Date Completed: 3/8/02
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: 1
AA Sequences: 1
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST(where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: QY
WWW/Internet: _____
Other (specify): _____

GenCore version 4.5

OM nucleic - nucleic search, using sw model

Run on: March 8, 2002, 08:51:10 ; Search time 2236.97 Seconds
(without alignments)
16939.888 Million cell updates/sec

Title: US-09-853-753-1
Perfect score: 2297
Sequence: 1 ggctgagggagtggaggggg.....aaggttaaaccggtttctct 2297

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
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2: gb_htg:*
3: gb_in:*
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9: gb_pr:*
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13: gb_un:*
14: gb_vi:*
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16: em_fun:*
17: em_hum:*
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24: em_pl:*
25: em_ro:*
26: em_sts:*
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32: em_htgo_rod:*
33: em_htg_hum:*
34: em_htg_inv:*
35: em_htg_rod:*
36: em_htg_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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2	2241	97.6	2713	9	HSA278865	AJ278865 Homo sapi
3	2163	94.2	133568	9	HS169I5	Z93015 Human DNA s
4	186	8.1	1818	9	S83462	S83462 ALS=85 kda
5	183.2	8.0	37635	9	AC004152	AC004152 Homo sapi
6	173.4	7.5	2125	9	HUMIGFACID	M86826 Human IGF b
7	173.4	7.5	4574	9	AF192554	AF192554 Homo sapi
8	173.4	7.5	21419	9	HS447E6	AL031724 Human DNA
9	161.2	7.0	251997	2	AC012180	AC012180 Homo sapi
10	147.8	6.4	128318	2	AC092532	AC092532 Papio cyn
11	145.6	6.3	157419	2	AC025389	AC025389 Homo sapi
12	144.6	6.3	1907	9	AB045987	AB045987 Macaca fa
13	143	6.2	1441	9	AF283463	AF283463 Homo sapi
14	143	6.2	1782	9	BC011787	BC011787 Homo sapi
15	143	6.2	2236	6	AX047642	AX047642 Sequence
16	143	6.2	2236	6	AX055398	AX055398 Sequence
17	143	6.2	168239	9	AC007663	AC007663 Homo sapi
18	143	6.2	174840	9	AC006549	AC006549 Homo sapi
19	143	6.2	184929	9	AC058790	AC058790 Homo sapi
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22	137.8	6.0	154277	2	AP003943	AP003943 Oryza sat
23	131.4	5.7	2621	9	AB046639	AB046639 Macaca fa
24	131.2	5.7	2382	6	AX156562	AX156562 Sequence
25	131.2	5.7	2636	6	AX156560	AX156560 Sequence
26	130.4	5.7	215727	2	AC073701	AC073701 Mus muscu
27	130.2	5.7	4933	9	AB014544	AB014544 Homo sapi
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34	126	5.5	3202	10	MMU66900	U66900 Mus musculu
35	126	5.5	175759	10	AF220294	AF220294 Mus muscu
36	125.2	5.5	130730	2	AL354712	AL354712 Homo sapi
37	125.2	5.5	159802	2	AC019262	AC019262 Homo sapi
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39	124	5.4	136198	2	AP003883	AP003883 Oryza sat
40	122.4	5.3	251997	2	AC012180	AC012180 Homo sapi
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43	119.2	5.2	3573	10	RNPLGPV	Z69594 R.norvegicu
44	119	5.2	1444	9	AF371328	AF371328 Homo sapi
45	117.8	5.1	1263	6	AX149553	AX149553 Sequence

ALIGNMENTS

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LOCUS AF254868 2297 bp mRNA PRI 28-DEC-2000
DEFINITION Homo sapiens nyctalopin mRNA, complete cds.
ACCESSION AF254868
VERSION AF254868.1 GI:11993320
KEYWORDS .
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2297)
AUTHORS Bech-Hansen,N.T., Naylor,M.J., Maybaum,T.A., Sparkes,R.L., Koop,B., Birch,D.G., Bergen,A.A., Prinsen,C.F., Polomeno,R.C., Gal,A., Drack,A.V., Musarella,M.A., Jacobson,S.G., Young,R.S. and Weleber,R.G.
TITLE Mutations in NYX, encoding the leucine-rich proteoglycan nyctalopin, cause X-linked complete congenital stationary night blindness
JOURNAL Nat. Genet. 26 (3), 319-323 (2000)

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  MEDLINE   20517340
   PUBMED   11062471
REFERENCE   2  (bases 1 to 2297)
  AUTHORS   Bech-Hansen,N.T., Maybaum,T.A. and Naylor,M.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-APR-2000) Medical Genetics, University of Calgary,
            3330 Hospital Dr. N.W., Calgary, AB T2N 4N1, Canada
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ORIGIN
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Query Match 100.0%; Score 2297; DB 9; Length 2297;
Best Local Similarity 100.0%; Pred. No. 1.1e-258;
Matches 2297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db   2281 GTTAAACCGGTTTCTCT 2297
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RESULT 2
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VERSION AJ278865.1 GI:11877211
KEYWORDS CLRP gene; leucine-rich repeat protein.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2713)
AUTHORS Pusch,C.M., Zeitz,C., Brandau,O., Pesch,K., Achatz,H., Feil,S., Scharfe,C., Maurer,J., Jacobi,F.K., Pinckers,A., Andreasson,S., Hardcastle,A., Wissinger,B., Berger,W. and Meindl,A.
TITLE The complete form of X-linked congenital stationary night blindness is caused by mutations in a gene encoding a leucine-rich repeat protein
JOURNAL Nat. Genet. 26 (3), 324-327 (2000)
MEDLINE 20517341
REFERENCE 2 (bases 1 to 2713)
AUTHORS Pusch,C.M.
TITLE Direct Submission
JOURNAL Submitted (23-AUG-2000) Medical Genetics, Ludwigs Maximilians University, Goethestr. 29, Munich D-80336, GERMANY
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    835 CACGCGCGCACCTTCGCGGCGCTCAGCCGCCTGCGCCGCCTAGACCTAGCAGCCTGCCGC 894

Qy    537 ctcttcagcgtgcccgagcgcctcctggccgaactgccggccctgcgcgaactcgccgcc 596
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    895 CTCTTCAGCGTGCCCGAGCGCCTCCTGGCCGAACTGCCGGCCCTGCGCGAACTCGCCGCC 954

Qy    597 ttcgacaacctgttccgccgcgtgccgggcgcgctgcgcggcctggccaacctgacgcac 656
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    955 TTCGACAACCTGTTCCGCCGCGTGCCGGGCGCGCTGCGCGGCCTGGCCAACCTGACGCAC 1014

Qy    657 gcgcacctggagcgcggccgcatcgaggcggtggcctccagctcgctgcagggcctgcgc 716
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1015 GCGCACCTGGAGCGCGGCCGCATCGAGGCGGTGGCCTCCAGCTCGCTGCAGGGCCTGCGC 1074

Qy    717 cgcctgcgctcgctcagcctgcaggccaaccgcgtccgtgccgtgcacgctggcgccttc 776
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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